Schreiber, David

Hi David Schreiber-
I was wondering if you could run the type of specialized search we discussed for antisense sequences,
wherein you rank ordered the hits using an Excel spreadsheet to pull up short, hit percent match hits for
09/676,436?
Could you please run a <u>length limited</u> nucleotide sequence search against nucleotides 3314-3333 of SEQ ID
NO:3 that returns hits 8-50 nucleotides then rank orders the hits based on percent complementarity over the
whole oligo, exactly as you performed previously? Please call me if there are any questions. The number of
hits to collect in the first round would be your best judgement.
Thanks,
Karen

Karen A. Lacourciere Ph.D.
CM1 11D09 GAU 1635
(703) 308-7523

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ ___   Examiner # : _____   Date: _____

Art Unit _____   Phone Number 30_____   Serial Number: _____

Mail Box and Bldg. Room Location _____   Results Format Preferred (circle):   PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.
****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention : _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date. _____

For Sequence Searches Only Please include all pertinent information *(parent, child, divisional, or issued patent numbers)* **along with the** appropriate serial number.

....

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher _____	NA Sequence (#)_____	STN _____
Searcher Phone # _____	AA Sequence (#)_____	Dialog _____
Searcher Location _____	Structure (#) _____	Questel Orbit _____
Date Searcher Received _____	Bibliographic _____	Online _____
Date Completed _____	Litigation _____	Lexis Nexis _____
Searcher Prep & Review Time _____	Full text _____	Sequence Systems _____
Clerical Prep Time _____	Patent Family _____	WWW Internet _____
_____ Time _____	Other _____	Other specify _____

_____

GenCore   version 5.1.6
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OM   nucleic -   nucleic using   sw   model

Run   on: Septem 30,   2003,   7:46:12 ;
        (without   alignments)
           199.182 Million   cell   updates/sec

Title: US-09-676-436-3_COPY_3314_3333
Perfect   score: 20
Sequenc   1 agggattcaggggttccagc 20

Scoring table: IDENTITY_NUC
         Gapop   10 ,   Gapex   1

Searched 33363688 seqs,   1.7E+10 residues

Total   number   of   hits   satisfy chosen   parameters 21323498

MinimumDB   seq   length: 8
MaximumDB   seq   length: 50

Post-prodMinimum   Match   0%
         Maximum   Match   100%
         Listing   first   65000 summaries

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Pred.	No.	is	the	number		of	results	predicted
score	greater	than	or	equal		to	the	score
and	is	derived	by	analysis		of	the	total

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Score/Length
c 1	20	100	20	1	PCT-US01-30549-12	1
c 2	20	100	20	2	PCT-US01-30549-12	1
c 3	20	100	20	29	US-09-676-436-12	1
c 4	20	100	20	51	US-10-371-474-12	1
c18928	10	50	10	19	US-09-336-376-2856	1

c18929	10	50	10	19 US-09-336-376-4653	1
517	12.4	62	14	10 US-08-591-486B-72	0.885714
518	12.4	62	14	19 US-09-341-700A-895	0.885714
c41067	9.4	47	11	50 US-10-320-210A-4	0.854545
c41068	9.4	47	11	50 US-10-320-210A-127	0.854545
c18930	10	50	12	22 US-09-528-209A-8913	0.833333

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OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 08:22:42 ; Search time 1924 Seconds
                       (without alignments)
                       25.878 Million cell updates/sec

Title: US-09-676-436-3_COPY_3314_3333
Perfect score: 20
Sequence: 1 agggattcaggggttccagc 20

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1678620 seqs, 1244745471 residues

Total number of hits satisfying chosen parameters: 1072644

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 65000 summaries

Database :   Published_Applications_NA:*
          1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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          3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
          4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
          5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
          6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
          7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
          8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
          9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
          10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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          12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
          13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
          14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
          15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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          17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

     Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Score/length
c 1	20	100	20	12	US-10-371-474-12	1
22	12.4	62	14	8	US-08-591-486B-72	0.885714
8396	8.4	42	10	9	US-09-989-789-1270	0.84
8397	8.4	42	10	9	US-09-989-789-1275	0.84
8398	8.4	42	10	9	US-09-989-789-1337	0.84
8399	8.4	42	10	11	US-09-990-186-1270	0.84
8400	8.4	42	10	11	US-09-990-186-1275	0.84
8401	8.4	42	10	11	US-09-990-186-1337	0.84
c8402	8.4	42	10	11	US-09-953-562-26	0.84
8403	8.4	42	10	11	US-09-989-994-1270	0.84
8404	8.4	42	10	11	US-09-989-994-1275	0.84
8405	8.4	42	10	11	US-09-989-994-1337	0.84
8406	8.4	42	10	12	US-10-330-627-435	0.84
8407	8.4	42	10	12	US-10-330-627-1496	0.84
8408	8.4	42	10	12	US-10-330-627-1546	0.84
c29527	7.4	37	9	9	US-09-955-518-18	0.822222
14156	8	40	10	12	US-10-330-627-588	0.8
c14157	8	40	10	13	US-10-033-145-524	0.8
14158	8	40	10	13	US-10-033-145-765	0.8
14159	8	40	10	13	US-10-033-145-1337	0.8

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OM nucleic - nucleic search, using sw mode!

Run on: September 30, 2003, 07:46:12 ; Search time 283 Seconds
                          (without alignments)
                          190.773 Million cell updates/sec

Title: US-09-676-436-3_COPY_3314_3333
Perfect score: 20
Sequence: 1 agggattcaggggttccagc 20

Scoring table: IDENTITY_NUC
          Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2466760

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
          Maximum Match 100%
          Listing first 65000 summaries

Database :   N_Geneseq_19Jun03:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Score/Length
c 1	20	100	20	24 AAD37150		1
c 427	11	55	11	24 ABV67711		1
c 428	11	55	11	24 ABQ87435		1
c1844	10	50	10	21 AAZ83859		1
c24566	8	40	8	21 AAA80926		1
c1845	10	50	11	24 ABV66038		0.909091
6903	9	45	10	21 AAC74212		0.9
c6904	9	45	10	21 AAZ83465		0.9
6905	9	45	10	21 AAZ84256		0.9
6906	9	45	10	22 AAF42053		0.9
c6907	9	45	10	24 AAL48142		0.9
c6908	9	45	10	24 ABK64082		0.9
40	12.4	62	14	16 AAQ83338		0.885714
c4115	9.4	47	11	24 AAL42209		0.854545
c4116	9.4	47	11	24 ABV62683		0.854545
4117	9.4	47	11	24 ABV68833		0.854545
c4118	9.4	47	11	24 ABV70104		0.854545
c4119	9.4	47	11	24 ABQ86371		0.854545
c14562	8.4	42	10	19 AAV35904		0.84
14563	8.4	42	10	21 AAC73982		0.84
14564	8.4	42	10	21 AAA56134		0.84
14565	8.4	42	10	21 AAA56289		0.84
14566	8.4	42	10	21 AAA56391		0.84
c14567	8.4	42	10	21 AAZ83394		0.84
c14568	8.4	42	10	21 AAZ83550		0.84
14569	8.4	42	10	21 AAZ84309		0.84
c14570	8.4	42	10	21 AAZ84773		0.84
c14571	8.4	42	10	21 AAZ85387		0.84
c14572	8.4	42	10	21 AAZ85591		0.84
c14573	8.4	42	10	21 AAZ85716		0.84
c14574	8.4	42	10	22 AAI67389		0.84
14575	8.4	42	10	22 AAS57315		0.84

14576	8.4	42	10	22 ABA06128	0.84
14577	8.4	42	10	22 AAH63595	0.84
14578	8.4	42	10	22 AAH64656	0.84
14579	8.4	42	10	22 AAH64706	0.84
c14580	8.4	42	10	22 AAH19941	0.84
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c14582	8.4	42	10	22 AAH32697	0.84
14583	8.4	42	10	22 AAF36987	0.84
14584	8.4	42	10	22 AAF39730	0.84
c14585	8.4	42	10	22 AAF41037	0.84
14586	8.4	42	10	24 ABQ71536	0.84
14587	8.4	42	10	24 ABQ71541	0.84
14588	8.4	42	10	24 ABQ71603	0.84
14589	8.4	42	10	24 ABK85685	0.84
14590	8.4	42	10	24 ABK23413	0.84
c14591	8.4	42	10	24 AAS19576	0.84
14592	8.4	42	10	24 ABL42689	0.84
c14593	8.4	42	10	24 ABL42751	0.84
c14594	8.4	42	10	24 ABL42815	0.84
c50539	7.4	37	9	19 AAV04711	0.822222
c6909	9	45	11	22 AAF30844	0.818182
6910	9	45	11	24 ABV63615	0.818182
6911	9	45	11	24 ABV64938	0.818182
c6912	9	45	11	24 ABV64961	0.818182
6913	9	45	11	24 ABV65456	0.818182
6914	9	45	11	24 ABV71036	0.818182
6915	9	45	11	24 ABQ87139	0.818182
24567	8	40	10	15 AAQ63560	0.8
c24568	8	40	10	21 AAZ78096	0.8
24569	8	40	10	21 AAZ78337	0.8
24570	8	40	10	21 AAZ78909	0.8
c24571	8	40	10	21 AAZ81683	0.8
c24572	8	40	10	21 AAZ82371	0.8
c24573	8	40	10	21 AAZ83968	0.8
24574	8	40	10	21 AAZ84127	0.8
24575	8	40	10	21 AAZ84157	0.8
c24576	8	40	10	21 AAZ84158	0.8
c24577	8	40	10	21 AAZ84257	0.8
c24578	8	40	10	21 AAZ84401	0.8
24579	8	40	10	21 AAZ84685	0.8
24580	8	40	10	21 AAZ85131	0.8
c24581	8	40	10	21 AAZ85236	0.8
24582	8	40	10	22 AAH63748	0.8
24583	8	40	10	22 AAF35691	0.8
c24584	8	40	10	22 AAF36466	0.8
c24585	8	40	10	22 AAF40055	0.8
24586	8	40	10	22 AAF42054	0.8
24587	8	40	10	22 AAF42057	0.8
24588	8	40	10	22 AAF42631	0.8

c24589	8	40	10	22	AAF42841	0.8
24590	8	40	10	24	AAD45882	0.8
c24591	8	40	10	24	ABK96539	0.8
c24592	8	40	10	24	ABK92637	0.8
24593	8	40	10	24	ABK14251	0.8
24594	8	40	10	24	ABK23538	0.8
24595	8	40	10	24	ABK23629	0.8
c24596	8	40	10	25	ABT14312	0.8

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OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 07:46:12 ; Search time 1801 Seconds
                          (without alignments)
                          454.299 Million cell updates/sec

Title: US-09-676-436-3_COPY_3314_3333
Perfect score: 20
Sequence: 1 agggattcaggggttccagc 20

Scoring table: IDENTITY_NUC
            Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 1314098

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
            Maximum Match 100%
            Listing first 65000 summaries

Database :   GenEmbl:*
        1: gb_ba:*
        2: gb_htg:*
        3: gb_in:*
        4: gb_om:*
        5: gb_ov:*
        6: gb_pat:*
        7: gb_ph:*
        8: gb_pl:*
        9: gb_pr:*
        10: gb_ro:*
        11: gb_sts:*
        12: gb_sy:*
        13: gb_un:*
        14: gb_vi:*
        15: em_ba:*
        16: em_fun:*
        17: em_hum:*
        18: em_in:*
        19: em_mu:*

20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Score/length
c 329	11	55	11	6	AX471613	1
c 330	11	55	11	6	AX628456	1
c1489	10	50	10	6	I84475	1
c1490	10	50	11	6	AX626783	0.909090909
5458	9	45	10	6	E39766	0.9
36	12.4	62	14	6	A42556	0.885714286
37	12.4	62	14	6	A88747	0.885714286
38	12.4	62	14	6	BD066260	0.885714286
c3262	9.4	47	11	6	AX470549	0.854545455
c3263	9.4	47	11	6	AX623428	0.854545455
3264	9.4	47	11	6	AX629578	0.854545455
c3265	9.4	47	11	6	AX630849	0.854545455
11538	8.4	42	10	6	AR303398	0.84
c11539	8.4	42	10	6	AR303424	0.84
c11540	8.4	42	10	6	AX112965	0.84
11541	8.4	42	10	6	AX152520	0.84
11542	8.4	42	10	6	AX153581	0.84

9-28-2000

11543	8.4	42	10	6	AX153631	0.84
11544	8.4	42	10	6	AX301326	0.84
11545	8.4	42	10	6	AX667821	0.84
11546	8.4	42	10	6	AX667826	0.84
11547	8.4	42	10	6	AX667888	0.84
11548	8.4	42	10	6	BD007762	0.84
c11549	8.4	42	10	6	BD007794	0.84
11550	8.4	42	10	6	BD083142	0.84
c11551	8.4	42	10	6	BD083204	0.84
c11552	8.4	42	10	6	BD083268	0.84
11553	8.4	42	10	6	E39536	0.84
11554	8.4	42	10	6	E54753	0.84
5459	9	45	11	6	AX471317	0.818181818
5460	9	45	11	6	AX624360	0.818181818
5461	9	45	11	6	AX625683	0.818181818
c5462	9	45	11	6	AX625706	0.818181818
5463	9	45	11	6	AX626201	0.818181818
5464	9	45	11	6	AX631781	0.818181818
19241	8	40	10	6	AR017955	0.8
19242	8	40	10	6	AR303474	0.8
c19243	8	40	10	6	AR303528	0.8
19244	8	40	10	6	AX152673	0.8
19245	8	40	10	6	AX301451	0.8
19246	8	40	10	6	AX301542	0.8
19247	8	40	10	6	AX719148	0.8

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OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 07:46:12 ; Search time 74 Seconds
                        (without alignments)
                        119.293 Million cell updates/sec

Title: US-09-676-436-3_COPY_3314_3333
Perfect score: 20
Sequence: 1 agggattcaggggttccagc 20

Scoring table: IDENTITY_NUC
             Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 741060

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
             Maximum Match 100%
             Listing first 65000 summaries

Database :   Issued_Patents_NA:*
             1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
             2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
             3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
             4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
             5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
             6: /cgn2_6/ptod.ata/2/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                        SUMMARIES
                           %
Result   Query
No.   Score Match Length DB   ID   Score/Length
----

c 955   10   50   10   1 US-07-704-288C-25   1
c 956   10   50   10   1 US-08-379-259-25   1

c11470	8	40	8	3 US-08-859-954-239	1
37837	7	35	8	3 US-08-859-954-32	0.875
c37838	7	35	8	3 US-08-859-954-240	0.875
c37839	7	35	8	3 US-08-859-954-292	0.875
c37840	7	35	8	3 US-09-063-450-8	0.875
c37841	7	35	8	3 US-09-398-499-15	0.875
37842	7	35	8	3 US-09-398-499-38	0.875
7013	8.4	42	10	4 US-09-508-753B-123	0.84
c7014	8.4	42	10	4 US-09-508-753B-149	0.84
c23020	7.4	37	9	2 US-08-899-324-6	0.822222
c23021	7.4	37	9	3 US-08-329-892B-6	0.822222
c23022	7.4	37	9	4 US-08-874-569B-18	0.822222
c23023	7.4	37	9	4 US-09-955-518-18	0.822222
11471	8	40	10	1 US-08-590-804-20	0.8
11472	8	40	10	4 US-09-508-753B-199	0.8
c11473	8	40	10	4 US-09-508-753B-253	0.8